SEQUENCE LISTING



1680

<110> Weber, Bernard H.F. Stoehr, Heidi <120> Novel retina-specific human proteins C7orf9, C12orf7, MPP4 and F379 <130> 033488-001 <140> US 09/995,793 <141> 2001-11-29 <150> 60/253,751 <151> 2000-11-29 <160> 71 <170> PatentIn version 3.1 <210> 1 <211> 2435 <212> DNA <213> Homo sapiens <220> <221> misc feature artificial sequence, Translation start at 209; stop at 2435 <223> <400> 1 60 qaqattttat cgggagcagt gaggtgactt tggcagctaa caggccacta gtatcctact aaagcttttg tctggatagg agcaacatgc atgtttacag tcttgcagtg tgctgagagc 120 tggtggccag tgggactgag tgagctgtgt gccgtgtatt gacccgcttc ctagtcctga 180 attectttea gaageteegg cagggaggat gatacagtea gacaaaggag cagatecace 240 agacaagaag gacatgaagc tttctacagc caccaatcca cagaatggcc tctcccagat 300 cctqaqqctt qtqctqcaaq aqctqaqtct qttctacagc agagatgtga atggagtgtg 360 tctcttgtac gatctcctcc actcgccgtg gcttcaggct ctgctaaaga tttatgactg 420 480 cctccaggaa tttaaagaaa agaaactagt tcctgccaca ccacatgcac aggtgttatc 540 ctatgaggta gtggagttat tacgtgaaac ccctacttcc cctgagatcc aagagctgag acaaatqctc caggctccac acttcaaggc cttgctcagt gcccatgaca cgatagctca 600 qaaaqatttt qaaccccttc tccctccact gccagacaat atccctgaga gtgaggaagc 660 720 aatqaqqatt qtttqtttaq tqaaaaacca acagcccctg ggagccacca tcaagcgcca 780 cqaqatqaca qqqqacatct tqqtqqccaq qatcatccac gqtqggctgg cggagagaag 840 tgggttgcta tatgctggag acaaactggt agaagtgaat ggagtttcag ttgagggact ggaccctgaa caagtgatcc atattctggc catgtctcga ggcacaatca tgttcaaggt 900 960 ggttccagtc tctgaccctc ctgtgaatag ccagcagatg gtgtacgtcc gtgccatgac 1020 tgagtactgg ccccaggagg atcccgacat cccctgcatg gacgctggat tgcctttcca 1080 gaagggggac atcctccaga ttgtggacca gaatgatgcc ctctggtggc aggcccgaaa 1140 aatotcagac cotgotacot gogotgggot tgtcccttct aaccaccttc tgaagaggaa gcaacgggaa ttctggtggt ctcagccgta ccagcctcac acctgcctca agtcaaccct 1200 atcaatttct atggaagaag aagatgacat gaagattgat gagaaatgtg tggaagcaga 1260 tgaagaaaca tttgaatctg aggaactttc agaagacaag gaggagtttg ttggctacgg 1320 1380 tcagaagttc tttatagctg gcttccgccg cagcatgcgc ctttgtcgca ggaagtctca 1440 cctcagcccg ctgcatgcca gtgtgtgctg caccggcagc tgctacagtg cagtgggtgc cccttacgag gaggtggtga ggtaccagcg acgcccttca gacaagtacc gcctcatagt 1500 1560 gctcatqqqa ccctctqqtq ttgqaqtaaa tqaqctcaqa agacaactta ttgaatttaa tcccagccat tttcaaagtg ctgtgccaca cactactcgt actaaaaaga gttacgaaat 1620

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aagagcaagt caaaaactac tgtattgctt tcagtggctt ctgcgtggga gagatctggg
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ttgggctggg ccaaggatct ctgatctcat tgtcctcctc ctcctttttg acccctctc
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 acagcataac aaactgtatt ttttccattt gtccaattaa gtctgtacta tccatatttt
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 tctatttctc ctaaaggatg aagacctaca agagatggaa aatttagccc aaagaatgga
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 aactcagttt ggccaatttt ttgatcatgt gattgtgaat gacagcttgc acgatgcatg
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Gly Val Cys Leu Leu Tyr Asp Leu Leu His Ser Pro Trp Leu Gln Ala
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Leu Leu Lys Ile Tyr Asp Cys Leu Gln Glu Phe Lys Glu Lys Lys Leu
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Val Pro Ala Thr Pro His Ala Gln Val Leu Ser Tyr Glu Val Val Glu
                8.5
                                     90
Leu Leu Arg Glu Thr Pro Thr Ser Pro Glu Ile Gln Glu Leu Arg Gln
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                                 105
Met Leu Gln Ala Pro His Phe Lys Ala Leu Leu Ser Ala His Asp Thr
        115
                             120
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Ile Ala Gln Lys Asp Phe Glu Pro Leu Pro Pro Leu Pro Asp Asn
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Ile Pro Glu Ser Glu Glu Ala Met Arg Ile Val Cys Leu Val Lys Asn
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                                         155
Gln Gln Pro Leu Gly Ala Thr Ile Lys Arg His Glu Met Thr Gly Asp
                165
                                     170
                                                         175
Ile Leu Val Ala Arg Ile Ile His Gly Gly Leu Ala Glu Arg Ser Gly
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Leu Leu Tyr Ala Gly Asp Lys Leu Val Glu Val Asn Gly Val Ser Val
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Glu Gly Leu Asp Pro Glu Gln Val Ile His Ile Leu Ala Met Ser Arg
                        215
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Gly Thr Ile Met Phe Lys Val Val Pro Val Ser Asp Pro Pro Val Asn
                    230
                                         235
Ser Gln Gln Met Val Tyr Val Arg Ala Met Thr Glu Tyr Trp Pro Gln
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Glu Asp Pro Asp Ile Pro Cys Met Asp Ala Gly Leu Pro Phe Gln Lys
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270

265

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Gly Asp Ile Leu Gln Ile Val Asp Gln Asn Asp Ala Leu Trp Trp Gln
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Ala Arg Lys Ile Ser Asp Pro Ala Thr Cys Ala Gly Leu Val Pro Ser
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Asn His Leu Leu Lys Arg Lys Gln Arg Glu Phe Trp Trp Ser Gln Pro
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                                        315
Tyr Gln Pro His Thr Cys Leu Lys Ser Thr Leu Ser Ile Ser Met Glu
                325
                                    330
Glu Glu Asp Asp Met Lys Ile Asp Glu Lys Cys Val Glu Ala Asp Glu
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Glu Thr Phe Glu Ser Glu Glu Leu Ser Glu Asp Lys Glu Glu Phe Val
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Gly Tyr Gly Gln Lys Phe Phe Ile Ala Gly Phe Arg Arg Ser Met Arg
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Leu Cys Arg Arg Lys Ser His Leu Ser Pro Leu His Ala Ser Val Cys
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Cys Thr Gly Ser Cys Tyr Ser Ala Val Gly Ala Pro Tyr Glu Glu Val
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                                    410
Val Arg Tyr Gln Arg Arg Pro Ser Asp Lys Tyr Arg Leu Ile Val Leu
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Met Gly Pro Ser Gly Val Gly Val Asn Glu Leu Arg Arg Gln Leu Ile
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Glu Phe Asn Pro Ser His Phe Gln Ser Ala Val Pro His Thr Thr Arg
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Thr Lys Lys Ser Tyr Glu Met Asn Gly Arg Glu Tyr His Tyr Val Ser
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Lys Glu Thr Phe Glu Asn Leu Ile Tyr Ser His Arg Met Leu Glu Tyr
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                                    490
Gly Glu Tyr Lys Gly His Leu Tyr Gly Thr Ser Val Asp Ala Val Gln
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Thr Val Leu Val Glu Gly Lys Ile Cys Val Met Asp Leu Glu Pro Gln
                            520
Asp Ile Gln Gly Val Arg Thr His Glu Leu Lys Pro Tyr Val Ile Phe
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                                            540
Ile Lys Pro Ser Asn Met Arg Cys Met Lys Gln Ser Arg Lys Asn Ala
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                                        555
Lys Val Ile Thr Asp Tyr Tyr Val Asp Met Lys Phe Lys Asp Glu Asp
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                                    570
Leu Gln Glu Met Glu Asn Leu Ala Gln Arg Met Glu Thr Gln Phe Gly
                                585
Gln Phe Phe Asp His Val Ile Val Asn Asp Ser Leu His Asp Ala Cys
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Ala Gln Leu Leu Ser Ala Ile Gln Lys Ala Gln Glu Glu Pro Gln Trp
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<210> 27 <211> 512 <212> DNA <213> Homo sapiens	
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gctattcaag aaaatagatg atgcagaatt gaaacaagaa aaataagaaa cctggagcct
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gtccctaaag ctgtggcctg taatctacaa atggctctat agcgaagacc acacggaaga
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gtagctacat acacttcatc agctatggat catcaacggc aatttttcct tgtcagtaca
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gctataatag tatcttgaaa gttgtaaaaa aattaaagca tatttgttac gtaaagttaa
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aatgattttt gtctgaataa aaaaaaagca ttgcaaatgc tttagaaatc tctgataatg
                                                                       420
gagagagaga cagaggaccc tcctcactac cctatataaa aatcattggc acagttacac
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ttaataaaaa aaattaaaca gaagagcacc ctgaaaaaca ttatgatgga aattaaatag
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tatgccagaa taacatggtt gacaaataag tgaacaagga ttaaaaatca cttacaaacg
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tgtttctgta caccetttct atcgtgtcaa atgttaatga atctgtgatc aattgaaatg
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taaatgtctg tgtaaaacta caaaataaaa actcttagac tttagggaga aaagaaaaag
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                                 25
                                                     30
Ser Asn Leu His Ser Lys Glu Asn Tyr Asp Lys Tyr Ser Glu Pro Arg
Gly Tyr Pro Lys Gly Glu Arg Ser Leu Asn Phe Glu Glu Leu Lys Asp
                        55
Trp Gly Pro Lys Asn Val Ile Lys Met Ser Thr Pro Ala Val Asn Lys
                                         75
                                                             80
Met Pro His Ser Phe Ala Asn Leu Pro Leu Arg Phe Gly Arg Asn Val
                85
                                    90
Gln Glu Glu Arg Ser Ala Gly Ala Thr Ala Asn Leu Pro Leu Arg Ser
                                105
                                                     110
Gly Arg Asn Met Glu Val Ser Leu Val Arg Arg Val Pro Asn Leu Pro
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                            120
Gln Arg Phe Gly Arg Thr Thr Ala Lys Ser Val Cys Arg Met Leu
                        135
                                             140
Ser Asp Leu Cys Gln Gly Ser Met His Ser Pro Cys Ala Asn Asp Leu
                    150
                                        155
Phe Tyr Ser Met Thr Cys Gln His Gln Glu Ile Gln Asn Pro Asp Gln
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Lys Gln Ser Arg Arg Leu Leu Phe Lys Lys Ile Asp Asp Ala Glu Leu
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Lys Gln Glu Lys
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                                                                      300
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                                                                      360
cqaqaaqqat qcatttatqq cttcrtqaaq tctttcctga cccccqatgc tgctgactat
                                                                      420
agagacaaag teteactatg ttgeteagge tggtettgaa eteetggeet caagegatee
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tggtaatatt ttccccwcca aattcttgtc ggatgccctc acagaattga gattatgtac
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                                                                      660
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ccaatggact ctgcatggga gtgacgcatg cwgcctccag gcttgtccct aaaacctccc
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ttagtgatgg cagaaccata gatgggagga acctgggtcc ctgacttaaa gtatcatgga
                                                                     1080
tttggatgtt cccttagtga gaaataaact tccattgtgt ttaagccttt atttgtttat
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                                25
Val Gly Ile Ile Asp Met Ser His Cys Thr Trp Pro Thr Leu Gly Lys
        35
                            40
Phe Leu Asn Pro Ser Lys Pro His Phe Ser Pro Ile Thr Lys Gly Lys
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Asp Gly Asn Ile Phe Pro Thr Lys Phe Leu Ser Asp Ala Leu Thr Glu
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Leu Arg Leu Cys Thr
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                                                                      180
tgtggaccct gtgccaggaa aggaagggcg cagctcctgc aatgcggagc agccagggca
gtgggcacca ggctttagcc tccctttctc accctacaga gggcaggccc ttcagctcca
                                                                      240
ttctcctcca aggctgcaga gggggcagga attgggggtg acaggagagc tgtaaggtct
                                                                      300
                                                                      360
ccagtgggtc attctgggcc cagagatggg tgctgaagct cccacgcctg cctgtgaaaa
tggagtecte teteacetgg gagageeagg tgetgeeeeg agaaggatge atttatgget
                                                                      420
tcatgaagtc tttcctgacc cccgatgctg ctgactatag gtaagtctga gcaaatctgg
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                                                                      120
qctcaqqctq qtcttqaact cctqqcctca aqcqatcctc ccaccttagc ctcccaaaga
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gttgggatta tagacatgag ccactgcacc tggccgacct tgggcaagtt cttaaaccct
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tcaaagcctc atttttctcc aatcataaaa gggaaagatg gtaatatttt cccctccaaa
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ttcttgtaag tattaaacat tgtatatgta ttttgaacac gattaagctc taaacacttg
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gcctgactga acattttctc cacctcctga tcatcagcag cagaaactgg ctgctcttcc
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tggaagaccc agattagtga tggcagaacc atagatggga ggaacctggg tccctgactt
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tttatttgtt tatagttggt tacagcaact gccttctttt aattaaaaca ctcctgctgc
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                                                                      180
catagatacc ctacgaaccc caaatgccag ctgcatgaga aaagggactc accttctggt
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cggcttccag agtgttgtgg ccctgctcag ccactgtcct ttccttgatg tgaaccagca
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ggggggtgtt ctggaccacc ttgtgactgc cacaaccagc ctggccagtc ccttcgtcac
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gaatggcaca gaagtagggg aagatgggat aggacaggct gggaacaggt aatcaggccc
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                                                                     1260
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taaatctgct ctcaacctat atatatacaa ggtcattcat tctagcattg tttgcaagag
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                                                                     1380
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                                                                      180
catagatace ctacgaacce caaatgecag etgeatgaga aaagggaete acettetggt
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